

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:

- 5 (a) a first nucleotide sequence encoding a first polypeptide comprising at least 100 amino acids, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 85% identity based on the Clustal alignment method,
- 10 (b) a second nucleotide sequence encoding a second polypeptide comprising at least 150 amino acids, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:34 have at least 70% identity based on the Clustal alignment method,
- 15 (c) a third nucleotide sequence encoding a third polypeptide comprising at least 180 amino acids, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 70% identity based on the Clustal alignment method,
- 20 (d) a fourth nucleotide sequence encoding a fourth polypeptide comprising at least 200 amino acids, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 70% identity based on the Clustal alignment method,
- 25 (e) a fifth nucleotide sequence encoding a fifth polypeptide comprising at least 200 amino acids, wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:32 have at least 85% identity based on the Clustal alignment method,
- 30 (f) a sixth nucleotide sequence encoding a sixth polypeptide comprising at least 210 amino acids, wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 70% identity based on the Clustal alignment method, or
- (g) the complement of the first, second, third, fourth, fifth, or sixth nucleotide sequence, wherein the complement and the first, second, third, fourth, fifth, or sixth nucleotide sequence contain the same number of nucleotides and are 100% complementary.

- 35 2. The polynucleotide of Claim 1, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:34 have at least 80% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 80% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20,

or SEQ ID NO:22 have at least 80% identity based on the Clustal alignment method, and wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 80% identity based on the Clustal alignment method.

5           3. The polynucleotide of Claim 1, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:34 have at least 85% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and  
10 the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 85% identity based on the Clustal alignment method, and wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 85% identity based on the Clustal alignment method.

15           4. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:34 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 90% identity based on the Clustal alignment method,  
20 wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of SEQ ID NO:32 have at least 90% identity based on the Clustal alignment method, and wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 90% identity based on the Clustal alignment method.

25           5. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:34 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 95% identity based on the Clustal alignment method,  
30 wherein the amino acid sequence of the fifth polypeptide and the amino acid sequence of  
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SEQ ID NO:32 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid sequence of the sixth polypeptide and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 95% identity based on the Clustal alignment method.

5           6. The isolated polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:2, wherein the second polypeptide comprises the amino acid sequence of SEQ ID NO:34, wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:14, wherein the fourth polypeptide comprises the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID  
10 NO:22, wherein the fifth polypeptide comprises the amino acid sequence of SEQ ID NO:32, and wherein the sixth polypeptide comprises the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40.

          7. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:1, wherein the second nucleotide  
15 sequence comprises the nucleotide sequence of SEQ ID NO:33, wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:13, wherein the fourth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:19, or SEQ ID NO:21, wherein the fifth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:32, and wherein the sixth nucleotide  
20 sequence comprises the nucleotide sequence of SEQ ID NO:27 or SEQ ID NO:39.

          8. The isolated polynucleotide of Claim 1, wherein the first, second, third, fourth, fifth, and sixth polypeptides are Dr1 or DRAP1 protein.

          9. A chimeric gene comprising the polynucleotide of Claim 1 operably linked to a regulatory sequence.

25           10. A vector comprising the polynucleotide of Claim 1.

          11. An isolated polynucleotide fragment comprising a nucleotide sequence comprised by the polynucleotide of Claim 1, wherein the nucleotide sequence contains at least 30 nucleotides.

          12. The fragment of Claim 11, wherein the nucleotide sequence contains at least  
30 40 nucleotides.

          13. The fragment of Claim 11, wherein the nucleotide sequence contains at least 60 nucleotides.

          14. An isolated polypeptide comprising:

          (a) a first amino acid sequence comprising at least 100 amino acids, wherein the  
35 first amino acid sequence and the amino acid sequence of SEQ ID NO:2 have at least 85% identity based on the Clustal alignment method,

- (b) a second amino acid sequence comprising at least 150 amino acids, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:34 have at least 70% identity based on the Clustal alignment method,
- (c) a third amino acid sequence comprising at least 180 amino acids, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 70% identity based on the Clustal alignment method,
- (d) a fourth amino acid sequence comprising at least 200 amino acids, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 70% identity based on the Clustal alignment method,
- (e) a fifth amino acid sequence comprising at least 200 amino acids, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:32 have at least 85% identity based on the Clustal alignment method, or
- (f) a sixth amino acid sequence comprising at least 210 amino acids, wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 70% identity based on the Clustal alignment method.

15. The polypeptide of Claim 14, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:34 have at least 80% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 80% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 80% identity based on the Clustal alignment method, and wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 80% identity based on the Clustal alignment method.

16. The polypeptide of Claim 14, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:34 have at least 85% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 85% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 85% identity based on the Clustal alignment method, and wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 85% identity based on the Clustal alignment method.

17. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 have at least 90% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of

SEQ ID NO:34 have at least 90% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 90% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 90% identity based on the Clustal alignment method, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:32 have at least 90% identity based on the Clustal alignment method, and wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 90% identity based on the Clustal alignment method.

18. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 have at least 95% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:34 have at least 95% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:14 have at least 95% identity based on the Clustal alignment method, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22 have at least 95% identity based on the Clustal alignment method, wherein the fifth amino acid sequence and the amino acid sequence of SEQ ID NO:32 have at least 95% identity based on the Clustal alignment method, and wherein the sixth amino acid sequence and the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40 have at least 95% identity based on the Clustal alignment method.

19. The polypeptide of Claim 14, wherein the first amino acid sequence comprises the amino acid sequence of SEQ ID NO:2, wherein the second amino acid sequence comprises the amino acid sequence of SEQ ID NO:34, wherein the third amino acid sequence comprises the amino acid sequence of SEQ ID NO:14, wherein the fourth amino acid sequence comprises the amino acid sequence of of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:20, or SEQ ID NO:22, wherein the fifth amino acid sequence comprises the amino acid sequence of SEQ ID NO:32, and wherein the sixth amino acid sequence comprises the amino acid sequence of SEQ ID NO:28 or SEQ ID NO:40.

20. The polypeptide of Claim 14, wherein the polypeptide is a Dr1 or DRAP1 protein.

21. A method for transforming a cell comprising introducing the polynucleotide of Claim 1 into a cell.

22. A cell comprising the chimeric gene of Claim 9.

23. A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of Claim 1 and regenerating a plant from the transformed plant cell.

24. A plant comprising the chimeric gene of Claim 9.

25. A seed comprising the chimeric gene of Claim 9.

26. A method for evaluating at least one compound for its ability to inhibit the activity of a protein involved in regulation of gene expression, the method comprising the steps of:

- 5 (a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a protein involved in regulation of gene expression, operably linked to at least one suitable regulatory sequence;
- (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the protein involved in regulation of gene expression  
10 encoded by the operably linked nucleic acid fragment in the transformed host cell;
- (c) optionally purifying the protein involved in regulation of gene expression expressed by the transformed host cell;
- (d) treating the protein involved in regulation of gene expression with a  
15 compound to be tested; and
- (e) comparing the activity of the protein involved in regulation of gene expression that has been treated with a test compound to the activity of an untreated protein involved in regulation of gene expression, thereby selecting compounds with potential for inhibitory activity.